

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/530,972
Source: PG
Date Processed by STIC: 3/9/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/530,972

CRF Edit Date: 3/9/06
Edited by: in

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☒ Deleted: ☒ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

☒ Other: corrected <1517 response



PCT

RAW SEQUENCE LISTING

DATE: 03/09/2006

PATENT APPLICATION: US/10/530,972

TIME: 16:49:59

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\03092006\J530972.raw

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3 <110> APPLICANT: Neose Technologies, Inc.
4     DeFrees, Shawn
5     Zopf, David
6     Bayer, Robert
7     Hakes, David
8     Chen, Xi
9     Bowe, Caryn
11 <120> TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF
12     ERYTHROPOIETIN
14 <130> FILE REFERENCE: 040853-01-5083US01
16 <140> CURRENT APPLICATION NUMBER: US 10/530,972
17 <141> CURRENT FILING DATE: 2005-04-11
19 <150> PRIOR APPLICATION NUMBER: PCT/US2003/031974
20 <151> PRIOR FILING DATE: 2003-10-08
22 <150> PRIOR APPLICATION NUMBER: PCT/US2002/32263
23 <151> PRIOR FILING DATE: 2002-10-09
25 <150> PRIOR APPLICATION NUMBER: US 10/410,945
26 <151> PRIOR FILING DATE: 2003-04-09
28 <150> PRIOR APPLICATION NUMBER: US 10/369,779
29 <151> PRIOR FILING DATE: 2003-03-17
31 <150> PRIOR APPLICATION NUMBER: US 10/360,770
32 <151> PRIOR FILING DATE: 2003-01-06
34 <150> PRIOR APPLICATION NUMBER: US 10/287,994
35 <151> PRIOR FILING DATE: 2002-11-05
37 <160> NUMBER OF SEQ ID NOS: 75
39 <170> SOFTWARE: PatentIn version 3.2
41 <210> SEQ ID NO: 1
42 <211> LENGTH: 525
43 <212> TYPE: DNA
44 <213> ORGANISM: Homo sapiens
46 <400> SEQUENCE: 1
47 acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg cttagagcaa      60
49 gtgaggaaga tccagggcga tggcgacgag ctccaggaga agctgtgtgc cacctacaag      120
51 ctgtgccacc ccgaggagct ggtgctgctc ggacactctc tgggcatccc ctgggctccc      180
53 ctgagcagct gccccagcca ggccctgcag ctggcaggct gcttgagcca actccatagc      240
55 ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc cgagttgggt      300
57 cccaccttgg acacactgca gctggacgct gccgactttg ccaccaccat ctggcagcag      360
59 atggaagaac tgggaatggc ccctgccctg cagcccaccc aggggtgcca gccggccttc      420
61 gcctctgctt tccagcgccg ggcaggaggg gtccctgggtg cctcccatct gcagagcttc      480
63 ctggaggtgt cgtaccgcgt tctacgccac cttgcccagc cctga                        525
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 174
67 <212> TYPE: PRT

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68 <213> ORGANISM: Homo sapiens

70 <400> SEQUENCE: 2

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71 Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
72 1          5          10          15
74 Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
75          20          25          30
77 Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
78          35          40          45
80 Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
81          50          55          60
83 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
84 65          70          75          80
86 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
87          85          90          95
89 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
90          100          105          110
92 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
93          115          120          125
95 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
96          130          135          140
98 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
99 145          150          155          160
101 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
102          165          170

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104 <210> SEQ ID NO: 3

105 <211> LENGTH: 1733

106 <212> TYPE: DNA

107 <213> ORGANISM: Homo sapiens

109 <400> SEQUENCE: 3

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112 tcaagttaag taaaatgtca atagcctttt aattttaattt ttaattgttt tatcattctt      120
114 tgcaataata aaacattaac tttatacttt ttaatttaat gtatagaata gagatataca      180
116 taggatatgt aaatagatac acagtgtata tgtgattaaa atataatggg agattcaatc      240
118 agaaaaaagt ttctaaaaag gctctggggg aaaagaggaa ggaaacaata atgaaaaaaa      300
120 tgtggtgaga aaaacagctg aaaacccatg taaagagtgt ataaagaaag caaaaagaga      360
122 agtagaaagt aacacagggg catttggaag atgtaaacga gtatgttccc tatttaaggc      420
124 taggcacaaa gcaaggctct cagagaacct ggagcctaag gtttaggctc acccatttca      480
126 accagtctag cagcatctgc aacatctaca atggccttga cctttgcttt actggtggcc      540
128 ctctggtgct tcagctgcaa gtcaagctgc tctgtgggct gtgatctgcc tcaaaccac      600
130 agcctgggta gcaggaggac cttgatgctc ctggcacaga tgaggagaat ctctcttttc      660
132 tctgcttga aggacagaca tgactttgga tttcccagg aggagtttgg caaccagttc      720
134 caaaaggctg aaaccatccc tgtcctccat gagatgatcc agcagatctt caatctcttc      780
136 agcaciaaagg actcatctgc tgcttgggat gagaccctcc tagacaaatt ctacactgaa      840
138 ctctaccagc agctgaatga cctggaagcc tgtgtgatac agggggtggg ggtgacagag      900
140 actcccctga tgaaggagga ctccattctg gctgtgagga aatacttcca aagaatcact      960
142 ctctatctga aagagaagaa atacagccct tgtgcctggg aggttgtcag agcagaaatc      1020
144 atgagatctt tttctttgtc aacaaacttg caagaaagtt taagaagtaa ggaatgaaaa      1080
146 ctggttcaac atggaaatga ttttcattga ttcgtatgcc agctcacctt tttatgatct      1140
148 gccatttcaa agactcatgt ttctgctatg accatgacac gatttaaate ttttcaaagt      1200

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150 tttttaggag tattaatcaa cattgtattc agctcttaag gcactagtcc cttacagagg 1260
152 accatgctga ctgatccatt atctatttaa atatttttaa aatattattt atttaactat 1320
154 ttataaaaca acttattttt gttcatatta tgtcatgtgc acctttgcac agtggttaat 1380
156 gtaataaaaat gtgttctttg tatttggtaa atttattttg tgttgttcat tgaacttttg 1440
158 ctatggaact tttgtacttg tttattcttt aaaatgaaat tccaagccta attgtgcaac 1500
160 ctgattacag aataactggt acacttcatt tgtccatcaa tattatattc aagatataag 1560
162 taaaaataaa ctttctgtaa accaagttgt atgttgact caagataaca gggatgaacct 1620
164 aacaaataca attctgctct cttgtgtatt tgatttttgt atgaaaaaaa ctaaaaatgg 1680
166 taatcatact taattatcag ttatggtaaa tggatgaag agaagaagga acg 1733

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168 <210> SEQ ID NO: 4

169 <211> LENGTH: 188

170 <212> TYPE: PRT

171 <213> ORGANISM: Homo sapiens

173 <400> SEQUENCE: 4

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174 Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
175 1 5 10 15
177 Lys Ser Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu
178 20 25 30
180 Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
181 35 40 45
183 Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
184 50 55 60
186 Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
187 65 70 75 80
189 Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
190 85 90 95
192 Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
193 100 105 110
195 Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
196 115 120 125
198 Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
199 130 135 140
201 Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
202 145 150 155 160
204 Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
205 165 170 175
207 Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
208 180 185

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210 <210> SEQ ID NO: 5

211 <211> LENGTH: 757

212 <212> TYPE: DNA

213 <213> ORGANISM: Homo sapiens

215 <400> SEQUENCE: 5

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216 atgaccaaca agtgtctcct ccaaattgct ctctgttgt gcttctccac tacagctctt 60
218 tccatgagct acaacttgct tggattccta caaagaagca gcaattttca gtgtcagaag 120
220 ctctgtggc aattgaatgg gaggttgaa tattgcctca aggacaggat gaactttgac 180
222 atccctgagg agattaagca gctgcagcag ttccagaagg aggacgccgc attgaccatc 240
224 tatgagatgc tccagaacat ctttgctatt ttcagacaag attcatctag cactggctgg 300
226 aatgagacta ttgttgagaa cctcctggct aatgtctatc atcagataaa ccatctgaag 360

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228 acagtcctgg aagaaaaact ggagaaagaa gattttacca ggggaaaact catgagcagt 420
230 ctgcacctga aaagatatta tgggaggatt ctgcattacc tgaaggccaa ggagtacagt 480
232 cactgtgcct ggaccatagt cagagtggaa atcctaagga acttttactt cattaacaga 540
234 cttacagggtt acctccgaaa ctgaagatct cctagcctgt ccctctggga ctggacaatt 600
236 gcttcaagca ttcttcaacc agcagatgct gtttaagtga ctgatggcta atgtactgca 660
238 aatgaaagga cactagaaga ttttgaaatt tttattaaat tatgagttat ttttatttat 720
240 ttaaatttta ttttgaaaaa taaattatth ttggtgc 757

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242 <210> SEQ ID NO: 6

243 <211> LENGTH: 187

244 <212> TYPE: PRT

245 <213> ORGANISM: Homo sapiens

247 <400> SEQUENCE: 6

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248 Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
249 1 5 10 15
251 Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
252 20 25 30
254 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
255 35 40 45
257 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
258 50 55 60
260 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
261 65 70 75 80
263 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
264 85 90 95
266 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
267 100 105 110
269 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
270 115 120 125
272 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
273 130 135 140
275 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
276 145 150 155 160
278 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
279 165 170 175
281 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
282 180 185

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284 <210> SEQ ID NO: 7

285 <211> LENGTH: 1332

286 <212> TYPE: DNA

287 <213> ORGANISM: Homo sapiens

289 <400> SEQUENCE: 7

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290 atggtctccc aggccctcag gctcctctgc cttctgcttg ggcttcaggg ctgcctggct 60
292 gcagtccttcg taaccagga ggaagccac ggcgtcctgc accggcgccg gcgcgccaac 120
294 gcgttctctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc 180
296 tccttcgagg aggcccgga gatcttcaag gacgcggaga ggacgaagct gttctggatt 240
298 tcttacagtg atggggacca gtgtgcctca agtccatgcc agaattggggg ctctgcaag 300
300 gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag 360
302 acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc 420
304 agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgctggca 480

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306 gacgggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa 540
308 aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaagggtgtg ccccaaaggg 600
310 gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg 660
312 atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg 720
314 aacctgatcg cggtgctggg cgagcacgac ctacgcgagc acgacgggga tgagcagagc 780
316 cggcgggtgg cgcaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac 840
318 atcgcgctgc tccgcctgca ccagcccgtg gtccctactg accatgtggt gcccctctgc 900
320 ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc 960
322 ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt gctcaacgtg 1020
324 ccccggtgta tgaccagga ctgcctgcag cagtcacgga aggtgggaga ctcccaaata 1080
326 atcacggagt acatgttctg tgccggctac tcggatggca gcaaggactc ctgcaagggg 1140
328 gacagtggag gccacatgc caccactac cggggcacgt ggtacctgac gggcatcgtc 1200
330 agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctccag 1260
332 tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gccaggagt cctcctgcga 1320
334 gccccatttc cc 1332
336 <210> SEQ ID NO: 8
337 <211> LENGTH: 444
338 <212> TYPE: PRT
339 <213> ORGANISM: Homo sapiens
341 <400> SEQUENCE: 8
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343 1 5 10 15
344 Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
345 20 25 30
347 Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
348 35 40 45
350 Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
351 50 55 60
353 Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
354 65 70 75 80
356 Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
357 85 90 95
359 Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
360 100 105 110
362 Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
363 115 120 125
365 Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
366 130 135 140
368 Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
369 145 150 155 160
371 Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
372 165 170 175
374 Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
375 180 185 190
377 Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
378 195 200 205
380 Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
381 210 215 220
383 Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg

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VERIFICATION SUMMARY

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